



003300-589.ST25

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## SEQUENCE LISTING

TECH CENTER 1600/2900

<110> ULF, Lindahl  
LI, Jin-Ping

<120> DNA Sequence Coding for a Mammalian Glucuronyl C5-Epimerase and a  
Process for Its Production

<130> 003300-589

<140> US 09/403,269

<141> 1999-10-18

<150> SE 9701454-2

<151> 1997-04-18

<150> PCT/SE98/00703

<151> 1998-04-17

<160> 13

<170> PatentIn version 3.0

<210> 1

<211> 17

<212> DNA

<213> Human

<400> 1

gctgattcctt ttctgtc

17

<210> 2

<211> 13

<212> PRT

<213> Human

<220>

<221> PEPTIDE

<222> (5)..(5)

<223> Amino acid 5 is Xaa wherein Xaa = any amino acid.

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Pro Asn Asp Trp Xaa Val Pro Lys Gly Cys Phe Met Ala  
1 5 10

<210> 3

<211> 11

<212> PRT

<213> Human

<220>

<221> PEPTIDE

<222> (2)..(10)

<223> Amino acids 2 and 10 are Xaa wherein Xaa = any amino acid.

&lt;400&gt; 3

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 1 5 10

<210> 4  
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 <222> (4)..(4)  
 <223> Amino acid 4 is Xaa wherein Xaa = any amino acid.

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Pro Asn Asp Xaa Thr Val Pro Lys  
 1 5

<210> 5  
 <211> 15  
 <212> PRT  
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<220>  
 <221> PEPTIDE  
 <222> (1)..(11)  
 <223> Amino acids 1, 2 and 11 are Xaa wherein Xaa = any amino acid.

&lt;400&gt; 5

Xaa Xaa Ile Ala Pro Glu Thr Ser Glu Gly Xaa Ser Leu Gln Leu  
 1 5 10 15

<210> 6  
 <211> 10  
 <212> PRT  
 <213> Human

&lt;400&gt; 6

Gly Gly Trp Pro Ile Met Val Thr Arg Lys  
 1 5 10

<210> 7  
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 <212> PRT  
 <213> Human

&lt;400&gt; 7

Phe Leu Ser Glu Gln His Gly Val  
 1 5

<210> 8  
 <211> 36

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 <222> (30)..(30)  
 <223> Amino acid 30 is Xaa wherein Xaa = any amino acid.

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Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly Thr Ile Tyr Asp  
 1 5 10 15

Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu Ala Xaa Trp Asp  
 20 25 30

Tyr His Thr Thr  
 35

<210> 9<211> 25<212> DNA<213> Human<220><221> misc\_feature<222>  
 (14)..(23)<223> Nucleotides 14, 20 and 23 are "n" wherein "n" = any  
 nucleotide.

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25

<210> 10  
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<220>  
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 <222> (14)..(17)  
 <223> Nucleotides 14 and 17 are "n" wherein "n" = any nucleotide.

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26

<210> 11  
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 <222> (11)..(11)  
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<212> DNA  
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                   1      5                  10  
                   Met Ser Phe Glu Gly Tyr Asn Val Glu Val Arg Asp Arg  
 gtc aag tgc ata agt ggg gtt gaa ggt gta cct tta tct aca cag tgg 159  
 Val Lys Cys Ile Ser Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp  
           15                  20                  25  
 gga cct caa ggc tat ttc tac cca atc cag att gca cag tat ggg tta 207  
 Gly Pro Gln Gly Tyr Phe Tyr Pro Ile Gln Ile Ala Gln Tyr Gly Leu  
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 Ser His Tyr Ser Lys Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val  
                   50                  55                  60  
 tat gaa aca gca gaa gac agg gac aaa aac agc aag ccc aat gac tgg 303  
 Tyr Glu Thr Ala Glu Asp Arg Asp Lys Asn Ser Lys Pro Asn Asp Trp  
                   65                  70                  75  
 act gtg ccc aag ggc tgc ttt atg gct agt gtg gct gat aag tca aga 351  
 Thr Val Pro Lys Gly Cys Phe Met Ala Ser Val Ala Asp Lys Ser Arg  
                   80                  85                  90  
 ttc acc aat gtt aaa cag ttc att gct cca gaa acc agt gaa ggt gta 399  
 Phe Thr Asn Val Lys Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val  
           95                  100                  105  
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 Ser Leu Gln Leu Gly Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu  
           110                  115                  120                  125  
 aag ttc tta aca aat gga agc gtg tct gtg gtt ctg gag acg aca gaa 495  
 Lys Phe Leu Thr Asn Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu  
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 Lys Asn Gln Leu Phe Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile  
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 Ala Phe Lys Glu Arg Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser  
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 tgg agc aca gtt acc cgg gac ctg gtc act gac ctc agg aaa gga gtg 639  
 Trp Ser Thr Val Thr Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val  
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aag gtg gtt agg ttg att gcg aaa ggg aag ggc ttc ctt gac aac att Lys Val Val Arg Leu Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile 210 215 220	735
acc atc tct acc aca gcc cac atg gct gcc ttc ttc gct gcc agt gac Thr Ile Ser Thr Thr Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp 225 230 235	783
tgg ctg gtg agg aac cag gat gag aaa ggc ggc tgg ccg att atg gtg Trp Leu Val Arg Asn Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val 240 245 250	831
acc cgt aag tta ggg gaa ggc ttc aag tct tta gag cca ggg tgg tac Thr Arg Lys Leu Gly Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr 255 260 265	879
tcc gcc atg gcc caa ggg caa gcc att tct aca tta gtc agg gcc tat Ser Ala Met Ala Gln Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr 270 275 280 285	927
ctc tta aca aaa gac cat ata ttc ctc aat tca gct tta agg gca aca Leu Leu Thr Lys Asp His Ile Phe Leu Asn Ser Ala Leu Arg Ala Thr 290 295 300	975
gcc cct tac aag ttt ctg tca gag cag cat gga gtc aag gct gtg ttt Ala Pro Tyr Lys Phe Leu Ser Glu Gln His Gly Val Lys Ala Val Phe 305 310 315	1023
atg aat aaa cat gac tgg tat gaa gaa tat cca act aca cct agc tct Met Asn Lys His Asp Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser 320 325 330	1071
ttt gtt tta aat ggc ttt atg tat tct tta att ggg ctg tat gac tta Phe Val Leu Asn Gly Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu 335 340 345	1119
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ggc tca gga acc atc tat gac ctc cgg cac ttc atg ctt ggc att gcc Gly Ser Gly Thr Ile Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala 385 390 395	1263
ccc aac ctg gcc cgc tgg gac tat cac acc acc cac atc aat caa ctg Pro Asn Leu Ala Arg Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu 400 405 410	1311
cag ctg ctt agc acc att gat gag tcc cca atc ttc aaa gaa ttt gtc	1359

Gln	Leu	Leu	Ser	Thr	Ile	Asp	Glu	Ser	Pro	Ile	Phe	Lys	Glu	Phe	Val	
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 <213> Human

<400> 13

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Ile Ser Gly Val Glu Gly Val Pro Leu Ser Thr Gln Trp Gly Pro Gln  
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 35 40 45

Ser Lys Asn Leu Thr Glu Lys Pro Pro His Ile Glu Val Tyr Glu Thr  
 50 55 60

Ala Glu Asp Arg Asp Lys Asn Ser Lys Pro Asn Asp Trp Thr Val Pro  
 65 70 75 80

Lys Gly Cys Phe Met Ala Ser Val Ala Asp Lys Ser Arg Phe Thr Asn  
 85 90 95

Val Lys Gln Phe Ile Ala Pro Glu Thr Ser Glu Gly Val Ser Leu Gln  
 100 105 110

Leu Gly Asn Thr Lys Asp Phe Ile Ile Ser Phe Asp Leu Lys Phe Leu  
 115 120 125

Thr Asn Gly Ser Val Ser Val Val Leu Glu Thr Thr Glu Lys Asn Gln  
 130 135 140

Leu Phe Thr Val His Tyr Val Ser Asn Thr Gln Leu Ile Ala Phe Lys  
 145 150 155 160

Glu Arg Asp Ile Tyr Tyr Gly Ile Gly Pro Arg Thr Ser Trp Ser Thr

165	170	175
Val Thr Arg Asp Leu Val Thr Asp Leu Arg Lys Gly Val Gly Leu Ser 180 185 190		
Asn Thr Lys Ala Val Lys Pro Thr Arg Ile Met Pro Lys Lys Val Val 195 200 205		
Arg Leu Ile Ala Lys Gly Lys Gly Phe Leu Asp Asn Ile Thr Ile Ser 210 215 220		
Thr Thr Ala His Met Ala Ala Phe Phe Ala Ala Ser Asp Trp Leu Val 225 230 235 240		
Arg Asn Gln Asp Glu Lys Gly Gly Trp Pro Ile Met Val Thr Arg Lys 245 250 255		
Leu Gly Glu Gly Phe Lys Ser Leu Glu Pro Gly Trp Tyr Ser Ala Met 260 265 270		
Ala Gln Gly Gln Ala Ile Ser Thr Leu Val Arg Ala Tyr Leu Leu Thr 275 280 285		
Lys Asp His Ile Phe Leu Asn Ser Ala Leu Arg Ala Thr Ala Pro Tyr 290 295 300		
Lys Phe Leu Ser Glu Gln His Gly Val Lys Ala Val Phe Met Asn Lys 305 310 315 320		
His Asp Trp Tyr Glu Glu Tyr Pro Thr Thr Pro Ser Ser Phe Val Leu 325 330 335		
Asn Gly Phe Met Tyr Ser Leu Ile Gly Leu Tyr Asp Leu Lys Glu Thr 340 345 350		
Ala Gly Glu Lys Leu Gly Lys Glu Ala Arg Ser Leu Tyr Glu Arg Gly 355 360 365		
Met Glu Ser Leu Lys Ala Met Leu Pro Leu Tyr Asp Thr Gly Ser Gly 370 375 380		
Thr Ile Tyr Asp Leu Arg His Phe Met Leu Gly Ile Ala Pro Asn Leu 385 390 395 400		



Ala Arg Trp Asp Tyr His Thr Thr His Ile Asn Gln Leu Gln Leu Leu  
405 410 415

Ser Thr Ile Asp Glu Ser Pro Ile Phe Lys Glu Phe Val Lys Arg Trp  
420 425 430

Lys Ser Tyr Leu Lys Gly Ser Arg Ala Lys His Asn  
435 440

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